1. (Original) An automated method for the measurement of residual protein in a cellular specimen, comprising:

(a) providing a plurality of stained subsamples from a cellular specimen;

(b) automatically selecting a Z position in each subsample for imaging a candidate object of interest;

(c) automatically obtaining a low magnification image of the candidate objects of interest comprising obtaining a plurality of pixels in each subsample;

(d) automatically filtering the candidate object of interest pixels in each subsample with a low pass filter;

(e) automatically morphologically processing the candidate object of interest pixels in each subsample to identify artifact pixels;

(f) automatically identifying the candidate object of interest in each subsample by eliminating pixels identified as artifact pixels;

(g) adjusting the apparatus to a higher magnification;

(h) automatically acquiring a higher magnification image of the subsample, at the location coordinates corresponding to the low magnification image, for each candidate object of interest identified in (f);

(i) automatically transforming pixels of the higher magnification image in a first color space to a second color space to differentiate higher magnification candidate object of interest pixels from background pixels;

(j) automatically identifying, at high magnification, an object of interest from the candidate object of interest pixels in the second color space; and

(k) automatically determining the optical density of the protein in a cell contained in a subsample, wherein the optical density is indicative of the residual component of a cellular protein.

2. (Original) The method of claim 1, wherein the first color space comprises red, green, and blue components for each pixel and the transforming step includes converting the red, blue and green components for each pixel in the first color space to pixel values in a hue, saturation, and intensity space.

3. (Original) The method of claim 2, wherein the hue, saturation, and intensity pixel values are compared to a threshold to identify pixels having a component value equal to or greater than said threshold as candidate object of interests pixels.

4. (Original) The method of claim 1, wherein the cellular protein is an enzyme.

5. (Original) The method of claim 4, wherein the enzyme is alkaline phosphatase (AP).

6. (Original) The method of claim 4, wherein the enzyme is acid phosphatase (AcP).

7. (Original) The method of claim 4, wherein the enzyme is "-naphthyl butyrate esterase.

8. (Original) The method of claim 1, wherein the cellular protein is assayed immunologically.

9. (Original) The method of claim 1, wherein the image is a color image.

10. (Original) The method of claim 1, wherein the image is a digital image.

11. (Original) A computer program, residing on a computer-readable medium, for obtaining images of subsamples of a cellular specimen, the computer program comprising instructions for causing a computer to:

(a) select a Z position for imaging a candidate object of interest in a subsample;

(b) obtain a low magnification image of the candidate object of interest comprising obtaining a plurality of pixels;

(c) filter the candidate object of interest pixels in each subsample with a low pass filter;

(d) morphologically process the candidate object of interest pixels in each subsample to identify artifact pixels;

(e) identify the candidate object of interest by eliminating pixels identified as artifact pixels;

(f) adjust the apparatus to a higher magnification;

(g) acquire a higher magnification image of the subsample, at the location coordinates corresponding to the low magnification image, for each candidate object of interest identified in (e);

(h) transform pixels of the higher magnification image in a first color space to a second color space to differentiate higher magnification candidate object of interest pixels from background pixels;

(i) identify, at higher magnification, an object of interest from the candidate object of interest pixels in the second color space; and

(j) score a protein level in the subsample by determining the optical density of the protein in a cell.

12. (Original) An automated method for the measurement of residual protein in a cellular specimen, comprising:

(a) providing a plurality of stained subsamples from a cellular specimen;

(b) automatically selecting a Z position in each subsample for imaging a candidate object of interest;

(c) automatically obtaining a low magnification image of the candidate objects of interest comprising obtaining a plurality of pixels in each subsample;

(d) automatically filtering the candidate object of interest pixels in each subsample with a low pass filter;

(e) automatically morphologically processing the candidate object of interest pixels in each subsample to identify artifact pixels;

(f) automatically identifying the candidate object of interest in each subsample by eliminating pixels identified as artifact pixels;

(g) adjusting the apparatus to a higher magnification;

(h) automatically acquiring a higher magnification image of the subsample, at the location coordinates corresponding to the low magnification image, for each candidate object of interest identified in (f);

(i) automatically transforming pixels of the higher magnification image in a first color space to a second color space to differentiate higher magnification candidate object of interest pixels from background pixels;

(j) automatically identifying, at high magnification, an object of interest from the candidate object of interest pixels in the second color space; and

(k) automatically identifying cells contained in a subsample and automatically determining the optical density of the protein in a cell contained in an identified cell, wherein the optical density is indicative of the residual component of a cellular protein.